

GenCore version 4.1
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1M protein - protein search, using SW model

Run on: September 13, 2002, 09:21:05 : Search time 13.05 seconds

(with all parameters)
743,313,000 cells/spades/sec

Title: ILE-LEU-ARG-GLY

Posttest score: 1.1186 4

Sequence: 11186 4

Scoring table: RUSUM62
Gapop 10.0, Gapext 0.5

Search: 23128 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 27

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA:
1: 1990-5-11 100.0 9 1 US-08-213-124-27
2: 1990-5-11 100.0 9 2 US-08-482-651-19
3: 1990-5-11 100.0 9 4 US-08-159-412-27
4: 1990-5-11 100.0 9 4 US-08-460-092-27
5: 1990-5-11 100.0 10 1 US-08-416-953-4
6: 1990-5-11 100.0 10 2 US-08-456-842-4
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12: 1990-5-11 100.0 18 3 US-08-244-292-11
13: 1990-5-11 100.0 18 4 US-09-516-701-14
14: 1990-5-11 100.0 19 1 US-08-672-671A-1
15: 1990-5-11 100.0 19 1 US-08-672-671A-1
16: 1990-5-11 100.0 68 4 US-09-177-219-19
17: 1990-5-11 100.0 70 4 US-09-467-954F-19
18: 1990-5-11 100.0 70 4 US-09-467-954F-19
19: 1990-5-11 100.0 70 4 US-09-467-954F-19
20: 1990-5-11 100.0 70 4 US-09-467-954F-19
21: 1990-5-11 100.0 70 4 US-09-467-954F-19
22: 1990-5-11 100.0 71 1 US-08-289-441-1
23: 1990-5-11 100.0 71 1 US-08-457-419-1
24: 1990-5-11 100.0 71 1 US-08-555-679-1
25: 1990-5-11 100.0 71 4 US-09-251-11-1
26: 1990-5-11 100.0 71 5 US-09-025-025-1
27: 1990-5-11 100.0 76 2 US-08-722-469-1

Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	9	1	Sequence 27, Appl
2	19	100.0	9	2	Sequence 18, Appl
3	19	100.0	9	4	Sequence 21, Appl
4	19	100.0	9	4	Sequence 21, Appl
5	19	100.0	10	1	Sequence 4, Appl
6	19	100.0	10	2	Sequence 2, Appl
7	19	100.0	10	2	Sequence 2, Appl
8	19	100.0	12	2	Sequence 37, Appl
9	19	100.0	18	2	Sequence 140, Appl
10	19	100.0	18	3	Sequence 107, Appl
11	19	100.0	18	3	Sequence 14, Appl
12	19	100.0	18	3	Sequence 112, Appl
13	19	100.0	18	4	Sequence 140, Appl
14	19	100.0	19	1	Sequence 11, Appl
15	19	100.0	19	1	Sequence 24, Appl
16	19	100.0	68	4	Sequence 158, Appl
17	19	100.0	70	4	Sequence 29, Appl
18	19	100.0	70	4	Sequence 65, Appl
19	19	100.0	70	4	Sequence 80, Appl
20	19	100.0	70	4	Sequence 89, Appl
21	19	100.0	70	4	Sequence 90, Appl
22	19	100.0	71	1	Sequence 13, Appl
23	19	100.0	71	1	Sequence 13, Appl
24	19	100.0	71	1	Sequence 13, Appl
25	19	100.0	71	4	Sequence 2, Appl
26	19	100.0	71	5	Sequence 2, Appl
27	19	100.0	76	2	Sequence 7, Appl

28 19 100.0 76 1 US-09-214-28-1
29 19 100.0 76 1 US-08-742-28-1
30 19 100.0 76 1 US-08-125-11-1
31 19 100.0 76 1 US-08-469-28-1
32 19 100.0 76 1 US-08-250-075-1
33 19 100.0 76 2 US-08-050-075-1
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36 19 100.0 76 2 US-08-050-075-1
37 19 100.0 76 2 US-08-050-075-1
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41 19 100.0 76 2 US-08-050-075-1
42 19 100.0 76 2 US-08-050-075-1
43 19 100.0 76 2 US-08-050-075-1
44 19 100.0 76 2 US-08-050-075-1
45 19 100.0 76 2 US-08-050-075-1

RESULTS

RESULT 1

US-08-213-124-27

Sequence 27, Application 07/04/18124

Patent No. 5693426

GENERAL INFORMATION

Applicant: Kahu, Madhu

Title of Invention: ILE-LEU-ARG-GLY AND RELATED ANALOGS

Field of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

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Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

Priority of Invention: ILE-LEU-ARG-GLY

FILING DATE: 06-JUN-1996
 CLASSIFICATION: 445
 ATTORNEY/AGENT INFORMATION:
 NAME: Park, Fredric R.
 REGISTRATION NUMBER: 35,646
 REFERENCE/AGENT NUMBER: 25731 29941,73
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 424-0792
 TELETYPE: 706141
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: xyz (details p4, 16)
 CLONE: 3E11
 US-08-600-092-21

Query Match 100.00% Score 194 Hh 10 Length 92
 Best Local Similarity 100.00% Prod. No. 117
 Matches 4 Constructive 0 Mismatch 0 Indels 0 Deletions 0

QY 1 HRO 4
 1111
 10 4 HRO 7

RESULT 5
 US-08-416-970-3
 Sequence 3, Application US/09416960
 Patent No. 5780036
 GENERAL INFORMATION:
 APPLICANT: CHISARI, FRANCIS V.
 TITLE OF INVENTION: PEPTIDES FOR INDUCING ANTI-XCT
 TITLE OF INVENTION: PEPTIDES FOR INDUCING ANTI-XCT
 NUMBER OF SEQUENCES: 11
 ADDRESSING ADDRESS:
 ADDRESS: Two Second and Townsend Kips
 STREET: One Market Plaza, Street
 CITY: San Francisco
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 3.31
 SOFTWARE: Patented Release #100 V0.00.0000
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/09416960
 FILING DATE: 06-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09
 FILING DATE:
 APPLICATION NUMBER: 09 07/99 05, 8992
 FILING DATE: 26 AUG 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09 07/99 05, 8992
 FILING DATE: 26 AUG 1992
 FILING DATE: 26 AUG 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Park, Fredric R.
 REGISTRATION NUMBER: 35,646
 REFERENCE/AGENT NUMBER: 25731 29941,73
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: xyz (details p4, 16)
 CLONE: 3E11
 US-08-416-970-3

Query Match 100.00% Score 194 Hh 10 Length 92
 Best Local Similarity 100.00% Prod. No. 117
 Matches 4 Constructive 0 Mismatch 0 Indels 0 Deletions 0

QY 1 HRO 4
 1111
 10 4 HRO 7

RESULT 6
 US-08-469-840-4
 Sequence 3, Application US/08469800
 Patent No. 5702224
 GENERAL INFORMATION:
 APPLICANT: CHISARI, FRANCIS V.
 TITLE OF INVENTION: PEPTIDES FOR INDUCING ANTI-XCT
 TITLE OF INVENTION: PEPTIDES FOR INDUCING ANTI-XCT
 NUMBER OF SEQUENCES: 11
 ADDRESSING ADDRESS:
 ADDRESS: Two Second and Townsend Kips
 STREET: One Market Plaza, Street
 CITY: San Francisco
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 3.31
 SOFTWARE: Patented Release #100 V0.00.0000
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08469800
 FILING DATE: 06-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/08469800
 FILING DATE:
 APPLICATION NUMBER: 08 07/99 05, 8992
 FILING DATE: 26 AUG 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08 07/99 05, 8992
 FILING DATE: 26 AUG 1992
 FILING DATE: 26 AUG 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Park, Fredric R.
 REGISTRATION NUMBER: 35,646
 REFERENCE/AGENT NUMBER: 25731 29941,73
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 467-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: xyz (details p4, 16)
 CLONE: 3E11
 US-08-469-840-4

Query Match 100.00% Score 194 Hh 10 Length 92
 Best Local Similarity 100.00% Prod. No. 117
 Matches 4 Constructive 0 Mismatch 0 Indels 0 Deletions 0

11-086-11
 September 14, 1994
 11-086-11

GENERAL INFORMATION

APPLICANT: 11-086-11

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APPLICANT: 11-086-11

APPLICANT: 11-086-11

APPLICANT: 11-086-11

FILING DATE: 28 JUN 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: WILNER, Mario S.
 REGISTRATION NUMBER: 42,161
 REFERENCE/PATENT NUMBER: 142-02641
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8000
 TELETYPE: 248345
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: Internal fragment
 US-06-672-571A-11

Query Match: 100.00; Score 19; E-Value 1.0e-04
 Best Local Similarity: 100.00; Pred. No. 7
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0
 QY: 1 EKG 4
 LB: 8 EKG 11

RESULT 15
 US-09-025-151-24
 Sequence 24; Application US/09025151
 Patent No. 6,187,545
 GENERAL INFORMATION:
 APPLICANT: Legrain, Pierre
 APPLICANT: Fromont, Michelle
 APPLICANT: Ratin, Jean-Christophe
 TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PEPTIDE
 TITLE OF INVENTION: POLYPEPTIDE INTERACTING WITH A RAIL POLYPEPTIDE OF
 TITLE OF INVENTION: INTERACTING POLYPEPTIDES
 TITLE OF INVENTION: INTERACTING POLYPEPTIDES
 FILE REFERENCE: 03495-0164
 CURRENT APPLICATION NUMBER: 09/202,2025,151
 CURRENT FILING DATE: 1998-02-18
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentID Ver. 2.0
 SEQ ID NO: 24
 LENGTH: 68
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-09-025-151-24

Query Match: 100.00; Score 19; E-Value 1.0e-04
 Best Local Similarity: 100.00; Pred. No. 2,800
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0
 QY: 1 EKG 4
 LB: 22 EKG 25

Search completed: September 13, 2002, 09:41:59
 Job time: 644 sec



[illegible]

GN PAG 3.

^aA new poly(ethylene terephthalate) was prepared by the reaction of terephthalic acid with ethylene glycol.

01-DEC-2001 (TREMBL) 19, Last annotated version

DE HYPOJERICAL 7.0 KDA PROTEIN.

GN Q26215.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nemata; Chromadorea; Eudelphia; Rhabditida; C

OC Rhabditidae; Polodrilae; Caenorhabditis.

OX NCBI_LuxID:6249

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN BRISTOL N2

FX MEDLINE 99069613; PubMed 9851915

RA None

RI "Genome sequence of the nematode *C. elegans*: a platform for

investigating biology. The *C. elegans* Sequencing Consortium."

RL Science 282:2282-2018(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN BRISTOL N2

RA In Z. Gilling S.

RI "The sequence of *C. elegans* coid Q26215

Submitted (09-1995) to the EMBL/Genbank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN BRISTOL N2

RA Waterston R.

RI "Direct Submission"

RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.

RF EMBL: M1557; AW24259.1

DR Hypothetical protein.

KW SEQUENCE 58 AA; 6988 MW; 434405419.400

SV

Query Match 100.00; Score 19; 13; 100.00; 58

Best Local Similarity 100.00; Ident. No. 1; 100.00; 58

Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 1187 4

DB 5 1187 8

RESULT 15

Q26174

ID Q26174 PROLIMINARY; PRT; 58 AA

AC Q26174

DI 01-NOV-1996 (TREMBL) 31, Cleaved

DI 01-NOV-1996 (TREMBL) 31, Last sequence 4177

DI 01-DEC-2001 (TREMBL) 19, Last annotated 4180

DE GAD1 PROTEIN (FRAGMENT).

GN GAD1

OS Plasmodium vivax

OC Eukaryota; Alveolata; Apicomplexa; Haemosporia; Sarcodina;

OC NCBI_LuxID 98453

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE 95059903; PubMed 7643772

RA Shewlin V.A.; Khouri E.; Muthuvallanage J.; P. J. Lee; Hromadova S.

RA Mendis K.N.; David P.H.

RI "A new polymorphic marker for PCR typing of *Plasmodium vivax*

parasites."

RL Mol. Biochem. Parasitol. 71:145-158(1995)

RF EMBL: X84573; CA559155.1

DI NON-DB

FI 1

FT NON-DB

ST 58

SV

SEQUENCE 58 AA; 6911 MW; 430344133.000

SV

Query Match 100.00; Score 19; 13; 100.00; 58

Best Local Similarity 100.00; Ident. No. 1; 100.00; 58

Matches 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 1187 4

DB 5 1187 8

DB 5 1187 8

Search completed: September 13, 2002 09:57:48
Job Time: 114 sec

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M protein - protein search, using SW model

[illegible]

Mathematical Analysis

III: E-ENT-ARZ-III

Stellen Sie sich vor, Sie sind ein Wissenschaftler, der die Eigenschaften von Materialien untersucht. Sie haben eine Reihe von Proben, die Sie in zwei Gruppen unterteilen möchten: eine Gruppe, die aus Materialien besteht, die eine bestimmte Eigenschaft haben, und eine Gruppe, die aus Materialien besteht, die diese Eigenschaft nicht haben. Sie haben eine Reihe von Proben, die Sie in zwei Gruppen unterteilen möchten: eine Gruppe, die aus Materialien besteht, die eine bestimmte Eigenschaft haben, und eine Gruppe, die aus Materialien besteht, die diese Eigenschaft nicht haben.

Figure 1. The structure of the *hsp70* gene. The gene is 1.2 kb in length. The exons are numbered 1 to 5. The introns are numbered 1 to 4. The positions of the primers used for PCR are indicated by arrows. The positions of the restriction sites for *Xba*I, *Hind*III, and *Eco*RI are indicated by asterisks.

Abstract

THE UNIVERSITY OF CHICAGO

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
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 127. **Tables**
 128. **Figures**
 129. **Supplementary Materials**
 130. **Author Contributions**
 131. **Funding**
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 249. **Conflicts of Interest**

$$\frac{f}{g} = \frac{\int_0^x f(t) dt}{\int_0^x g(t) dt}$$

105224 Eqs., 88719, 105110 =

Total number of hits satisfying criterion parameter α

THE SQUAT

Maximum dB Sec: 2000000000

Fast - Flocking Minimum Match

Maximilian Mathias

Database : SwissProt_40:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

CONCLUSIONS

Result	No.	Score	Quarter Match Length	Time	Tagset (p1,p2)
1	19	100-0	34	1	LENN_BROWN
2	19	100-0	43	1	HOSHI_ANEST
3	19	100-0	52	1	VERE_FOULI
4	19	100-0	63	1	VERE_FOULI
5	19	100-0	75	1	VERE_FOULI
6	19	100-0	86	1	VERE_FOULI
7	19	100-0	97	1	VERE_FOULI
8	19	100-0	96	1	VERE_FOULI
9	19	100-0	94	1	VERE_FOULI
10	19	100-0	99	1	VERE_FOULI
11	19	100-0	101	1	VERE_FOULI
12	19	100-0	105	1	VERE_FOULI
13	19	100-0	167	1	VERE_FOULI
14	19	100-0	116	1	VERE_FOULI
15	19	100-0	117	1	VERE_FOULI
16	19	100-0	122	1	VERE_FOULI
17	19	100-0	125	1	VERE_FOULI
18	19	100-0	129	1	VERE_FOULI
19	19	100-0	130	1	VERE_FOULI
20	19	100-0	142	1	VERE_FOULI
21	19	100-0	144	1	VERE_FOULI
22	19	100-0	145	1	VERE_FOULI
23	19	100-0	145	1	VERE_FOULI
24	19	100-0	145	1	VERE_FOULI
25	19	100-0	146	1	VERE_FOULI
26	19	100-0	147	1	VERE_FOULI
27	19	100-0	147	1	VERE_FOULI
28	19	100-0	147	1	VERE_FOULI
29	19	100-0	148	1	VERE_FOULI
30	19	100-0	148	1	VERE_FOULI
31	19	100-0	149	1	VERE_FOULI
32	19	100-0	149	1	VERE_FOULI
33	19	100-0	150	1	VERE_FOULI
34	19	100-0	150	1	VERE_FOULI
35	19	100-0	150	1	VERE_FOULI
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95	19	100-0	150	1	VERE_FOULI
96	19	100-0	150	1	VERE_FOULI
97	19	100-0	150	1	VERE_FOULI
98	19	100-0	150	1	VERE_FOULI
99	19	100-0	150	1	VERE_FOULI
100	19	100-0	150	1	VERE_FOULI

Run	Time	Altitude	Latitude	Longitude	Temperature	Humidity	Wind Speed	Wind Direction	Cloud Cover	Visibility	Pressure	Relative Humidity	Soil Moisture	Soil Temperature	Plant Growth	Notes
1	10:00	1000	35°N	140°E	25.0	65%	10	SE	10%	1000	1010	65%	10%	20.0	10	Good
2	11:00	1000	35°N	140°E	26.0	60%	12	SE	15%	1000	1010	60%	15%	21.0	12	Good
3	12:00	1000	35°N	140°E	27.0	55%	15	SE	20%	1000	1010	55%	20%	22.0	15	Good
4	13:00	1000	35°N	140°E	28.0	50%	18	SE	25%	1000	1010	50%	25%	23.0	18	Good
5	14:00	1000	35°N	140°E	29.0	45%	20	SE	30%	1000	1010	45%	30%	24.0	20	Good
6	15:00	1000	35°N	140°E	30.0	40%	22	SE	35%	1000	1010	40%	35%	25.0	22	Good
7	16:00	1000	35°N	140°E	31.0	35%	25	SE	40%	1000	1010	35%	40%	26.0	25	Good
8	17:00	1000	35°N	140°E	32.0	30%	28	SE	45%	1000	1010	30%	45%	27.0	28	Good
9	18:00	1000	35°N	140°E	33.0	25%	30	SE	50%	1000	1010	25%	50%	28.0	30	Good
10	19:00	1000	35°N	140°E	34.0	20%	32	SE	55%	1000	1010	20%	55%	29.0	32	Good
11	20:00	1000	35°N	140°E	35.0	15%	35	SE	60%	1000	1010	15%	60%	30.0	35	Good
12	21:00	1000	35°N	140°E	36.0	10%	38	SE	65%	1000	1010	10%	65%	31.0	38	Good
13	22:00	1000	35°N	140°E	37.0	5%	40	SE	70%	1000	1010	5%	70%	32.0	40	Good
14	23:00	1000	35°N	140°E	38.0	0%	42	SE	75%	1000	1010	0%	75%	33.0	42	Good
15	00:00	1000	35°N	140°E	39.0	0%	45	SE	80%	1000	1010	0%	80%	34.0	45	Good

[illegible]

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GenCore version 4.5
Copyright (c) 1993 - 2000 Emp. Inc.

ORF Protein - Protein search, using 2% match

Run on: September 13, 2002, 09:24:16 Search time: 0.13 Seconds

(447 total alignments)
25.137 bit from roll updates/sec

Title: lle-leu-arg-gly
Perfect score: 19
Sequence: 1 ILRG 4

Scoring table:
BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28219 seqs, 669924 residues

Total number of hits satisfying chosen parameters: 45/138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR21**
1: pir1**
2: pir2**
3: pir3**
4: pir4**

Result N is the number of results from total number of hits
score greater than or equal to the score of the result being printed,
and is divided by number of the total results distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	34	2 A4098	leader peptide (aa
2	19	100.0	39	2 G85837	hypothetical prote
3	19	100.0	43	2 S29763	antipeptidase N -
4	19	100.0	43	2 A32041	antitrial protein
5	19	100.0	50	2 T31019	hypothetical prote
6	19	100.0	51	2 S55419	GM1 protein - pla
7	19	100.0	52	2 T08487	hypothetical prote
8	19	100.0	52	2 A60410	hypothetical prote
9	19	100.0	53	2 B83853	hypothetical prote
10	19	100.0	57	2 S55452	GM1 protein - pla
11	19	100.0	58	2 T44120	hypothetical prote
12	19	100.0	61	2 F81510	hypothetical prote
13	19	100.0	62	2 T92371	hypothetical prote
14	19	100.0	68	2 S55454	GM1 protein - pla
15	19	100.0	68	2 S55455	GM1 protein - pla
16	19	100.0	69	1 P61486	home exporter prot
17	19	100.0	69	2 C01014	home exporter prot
18	19	100.0	69	2 A85859	home exporter prot
19	19	100.0	70	2 A60660	home exporter prot
20	19	100.0	70	2 A70787	home exporter prot
21	19	100.0	75	2 B70236	hypothetical prote
22	19	100.0	75	2 B97542	hypothetical prote
23	19	100.0	75	2 A52701	hypothetical prote
24	19	100.0	76	2 G70904	hypothetical prote
25	19	100.0	77	2 L51529	interactin alpha V-1
26	19	100.0	77	2 S48322	SHG protein - yoa
27	19	100.0	77	2 A00348	hypothetical prote
28	19	100.0	77	2 A72348	hypothetical prote
29	19	100.0	79	2 S55156	GM1 protein - pla

30	19	100.0	82	2 A02707	hypothetical prote
31	19	100.0	83	2 A02416	hypothetical prote
32	19	100.0	85	2 D11100	hypothetical prote
33	19	100.0	87	2 D04178	hypothetical prote
34	19	100.0	89	2 A02210	hypothetical prote
35	19	100.0	92	2 S55451	GM1 protein - pla
36	19	100.0	96	2 S09252	hypothetical prote
37	19	100.0	96	2 L41106	hypothetical prote
38	19	100.0	97	2 B05839	hypothetical prote
39	19	100.0	97	2 S09439	hypothetical prote
40	19	100.0	97	2 S08155	hypothetical prote
41	19	100.0	97	2 A72927	hypothetical prote
42	19	100.0	99	2 S05661	hypothetical prote
43	19	100.0	104	2 E70541	hypothetical prote
44	19	100.0	105	2 S09769	hypothetical prote
45	19	100.0	105	2 L10514	hypothetical prote

SUMMARIES

Result 1

A4098

leader peptide (aa

Species: Proteus vulgaris

Update: 10 Jun 1999 #sequence revision 18 Nov 2001 new chain 24 S.F. 100

Accession: A4098

Ekmanth, A.V.: Yacobsky, A.

J. Biol. Chem. 267, 1997-1996, 1992

A>Title: Characterization of the typhlopharyngeal protein for the development of a vaccine

A'Accession: A4098

A>Status: preliminary

A'Accession: A4098

A'Molecule type: nucleic acid

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1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 5. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0
 6. Amino acid sequence: Ile-Leu-Arg-Gly
 7. Molecular weight: 400.07
 8. pI: 4.0
 9. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 10. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0

1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 5. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0

1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
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1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 5. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0

1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 5. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0

1. Amino acid sequence: Ile-Leu-Arg-Gly
 2. Molecular weight: 400.07
 3. pI: 4.0
 4. Amino acid composition: Ile: 1, Leu: 1, Arg: 1, Gly: 1
 5. Amino acid analysis: Ile: 1.0, Leu: 1.0, Arg: 1.0, Gly: 1.0



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100.0	9	19	A

Description

1	19	100.0	5	21	AAV87478	Anti-bovine Yamana
2	19	100.0	6	22	AAV87502	Anti-bovine Yamana
3	19	100.0	6	23	AAV87527	Anti-bovine Yamana
4	19	100.0	9	19	AAV138609	Anti-bovine Yamana
5	19	100.0	9	15	AAV782749	Anti-bovine Yamana
6	19	100.0	9	15	AAV782751	Anti-bovine Yamana
7	16	100.0	6	16	AAV70066	Anti-bovine Yamana
8	19	100.0	9	16	AAV70075	Anti-bovine Yamana
9	19	100.0	9	18	AAV304550	Anti-bovine Yamana
10	19	100.0	9	19	AAV10786	Anti-bovine Yamana
11	19	100.0	9	19	AAV67106	Anti-bovine Yamana

12	1.2	1.9	1.90	0	1	1	AAW6746
13	1.3	1.9	1.90	0	1	1	AAW6707
14	1.4	1.9	1.90	0	1	1	AAW5450
15	1.5	1.9	1.90	0	1	1	AAW4547
16	1.6	1.9	1.90	0	1	1	AAW4000
17	1.7	1.9	1.90	0	1	1	AAW4461
18	1.8	1.9	1.90	0	1	1	AAW4645
19	1.9	1.9	1.90	0	1	1	AAW4650
20	2.0	1.9	1.90	0	1	1	AAW10577
21	2.1	1.9	1.90	0	1	1	AAW796
22	2.2	1.9	1.90	0	1	1	AAW4442
23	2.3	1.9	1.90	0	1	1	AAW1844
24	2.4	1.9	1.90	0	1	1	AAW6094
25	2.5	1.9	1.90	0	1	1	AAW3801
26	2.6	1.9	1.90	0	1	1	AAW6152
27	2.7	1.9	1.90	0	1	1	AAW7004
28	2.8	1.9	1.90	0	1	1	AAW6732
29	2.9	1.9	1.90	0	1	1	AAW6692
30	3.0	1.9	1.90	0	1	1	AAW6796
31	3.1	1.9	1.90	0	1	1	AAW8779
32	3.2	1.9	1.90	0	1	1	AAW6697
33	3.3	1.9	1.90	0	1	1	AAW4888
34	3.4	1.9	1.90	0	1	1	AAW7805
35	3.5	1.9	1.90	0	1	1	AAW4809
36	3.6	1.9	1.90	0	1	1	AAW7806
37	3.7	1.9	1.90	0	1	1	AAW7806
38	3.8	1.9	1.90	0	1	1	AAW7806
39	3.9	1.9	1.90	0	1	1	AAW7806
40	4.0	1.9	1.90	0	1	1	AAW7806
41	4.1	1.9	1.90	0	1	1	AAW7806
42	4.2	1.9	1.90	0	1	1	AAW7806
43	4.3	1.9	1.90	0	1	1	AAW7806
44	4.4	1.9	1.90	0	1	1	AAW7806
45	4.5	1.9	1.90	0	1	1	AAW7806
46	4.6	1.9	1.90	0	1	1	AAW7806
47	4.7	1.9	1.90	0	1	1	AAW7806
48	4.8	1.9	1.90	0	1	1	AAW7806
49	4.9	1.9	1.90	0	1	1	AAW7806
50	5.0	1.9	1.90	0	1	1	AAW7806

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RESULT 1
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THE UNIVERSITY OF CHICAGO

Аннотация

Education

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1.

Field	Modified-site	5
Field	Modified-site	5

[illegible]
$$\mathbb{Y}_{x_1, x_2}$$

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Prevention

Modified-site χ^2 /ndof = 1.16, minimum χ^2 = 1.16

JP3023790-B1

21 MAR - 2000.

31-MAY-1995;

31 Oct 1999

Figure 1

305

Gene Amy-Jeff

Query Match 100.000 Score 192.146 Length 81
 Host Local Similarity 100.000 Pos. No. 1-81
 Match 4. Conservation by Mismatch

QY 1 ILK 4
 1111
 1114 4

RESULT 4
 AAR78009
 ID AAR78009 standard: peptide 9 AA.

XX AAR78009
 XX 29-SEP-1999 (1.1st entry)

XX Influenza virus derived HLA-binding pep

XX Immunogen: H1A1 human leukocyte antigen H1A1 peptide and peptide

XX H1A1 and H1A2 (H1A1: 1-100, H1A2: 1-100) (H1A1: 1-100, H1A2: 1-100)

XX Protein: H1A1 (H1A1: 1-100, H1A2: 1-100) (H1A1: 1-100, H1A2: 1-100)

XX Influenza virus.

XX W09402205-A1.

XX 17-FEB-1994.

XX 06-AUG-1993: 73W0-0807421.

XX 05-MAR-1993: 940S-0027746.

XX 07-AUG-1992: 940S-0926566.

XX (CYTE) CYTEL CORP.

XX Cells E, Grey HM, Koko RT, Sette A.

XX WPI: 1994-065402/08.

XX Peptide which specifically binds select T cell clones used to
 XX induce an immune response for treatment of infection of viral
 XX infection or cancer, or for diagnosis

XX Description: Page 105: 150pp: English.

XX The sequence is a specific example of a group of new immunogenic
 XX peptides having an HLA-A2, HLA-A1, H1A1, H1A2, H1A3, H1A4, H1A5, H1A6, H1A7, H1A8, H1A9, H1A10, H1A11, H1A12, H1A13, H1A14, H1A15, H1A16, H1A17, H1A18, H1A19, H1A20, H1A21, H1A22, H1A23, H1A24, H1A25, H1A26, H1A27, H1A28, H1A29, H1A30, H1A31, H1A32, H1A33, H1A34, H1A35, H1A36, H1A37, H1A38, H1A39, H1A40, H1A41, H1A42, H1A43, H1A44, H1A45, H1A46, H1A47, H1A48, H1A49, H1A50, H1A51, H1A52, H1A53, H1A54, H1A55, H1A56, H1A57, H1A58, H1A59, H1A60, H1A61, H1A62, H1A63, H1A64, H1A65, H1A66, H1A67, H1A68, H1A69, H1A70, H1A71, H1A72, H1A73, H1A74, H1A75, H1A76, H1A77, H1A78, H1A79, H1A80, H1A81, H1A82, H1A83, H1A84, H1A85, H1A86, H1A87, H1A88, H1A89, H1A90, H1A91, H1A92, H1A93, H1A94, H1A95, H1A96, H1A97, H1A98, H1A99, H1A100, H1A101, H1A102, H1A103, H1A104, H1A105, H1A106, H1A107, H1A108, H1A109, H1A110, H1A111, H1A112, H1A113, H1A114, H1A115, H1A116, H1A117, H1A118, H1A119, H1A120, H1A121, H1A122, H1A123, H1A124, H1A125, H1A126, H1A127, H1A128, H1A129, H1A130, H1A131, H1A132, H1A133, 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